

# SEQ ID NO:16

## Rat Smooth Muscle Myosin Heavy Chain Gene Sequence (-4,216 to +11,795)

Nucleotide 1 corresponds to -4,216 bp relative to the SM-MHC transcription start site

5	AGATCTTAAA	ACACATCAAC	CTGGGCTGAG	GGGATGTGTG	TCTCTGTGTC	TGTGTATGCA	60
	CATGCATTTG	AGGCCAGATG	AAAATGTGAG	ATGTCCCTCTC	ACTGCTTTAT	TCCTCTGAGA	120
	CAGGGTCCCT	CAGTGAACCT	GTTGGAGCTA	TGCTGGTAGC	CAGCAAGCCC	CAGTGGCCCTT	180
10	CCTGTCTCTA	TCTCACACAG	CACAATATGT	GTGGCCGATG	TCCACTTTTT	TACATGGAAA	240
	TTGGGGTCTT	CCAACCTGGG	TTCTCATTTG	TGCAGTGACA	CTCTTCCCCA	CTGAGCCATC	300
	TCCTCAGGCC	AGCTGTATATA	TTTTTAAATA	ATTTAAATATT	TAGCACTATG	CTTTAGAAGC	360
	CAATAGCTAT	TTAAAGCTGT	TTGCTTTAAAA	AAAAAAGAAA	AAAAAAGACT	TCATTTATCC	420
	AACACTTTATG	AGGGAGAGAC	AATAATTTCCA	AAACCAGAAC	CAGCCAGGGT	ACACAGTGAG	480
15	ACTTTATTTA	AAAAAAGAAA	AAAAAGAAAG	AAAGAAAAAA	AAAAAAGAAA	GAAAAAAGAA	540
	GGCTCCAAAG	AGAAATTTCC	CCTTCATCAT	CTAATCACAA	GAACAACATT	TATTTATGTT	600
	GACATCACTC	AGTCCAAAGG	AGCTTTTGTG	AAAGTGACTT	CTCTTCTTAA	AATAAGTGAC	660
	CCTTCCCAAC	CACCAAAAAC	AAAAACAGAA	CCTCTGCCCT	GTTCAGAGT	CCTTTTGAAG	720
	ACTTTCAGATA	CCTGAAGAGT	GGACAGATAT	TTACCGAGTG	ACTTAAATGA	ACATACTGTC	780
20	CCTGGGTACT	GCTCAAGCAT	GCAGGAGAG	CATGGAATGT	TTATGCAAGG	CTGGCACTGT	840
	CATTACAAC	TCAGTAAGCG	GGAGAAGACA	GAGAGCCTCT	CCTAAGACAA	TGGCACATAA	900
	GGACATGGGT	AACCCAGAG	GTTCGCCGCT	AGTACTTAGC	AGAGCTGAGA	TCAGACTTGG	960
	GCCTCTGTGC	TGCTTGTGCT	AGTGGGCAAC	ATCTAAGACT	GGGGTAAACA	ATAAGTTGAT	1020
	CTGGGATATG	TGCTCAGTAA	CACACTTGAG	ATTCAACACT	GGGAAGGCAG	AGGAGATCC	1080
25	CTGGGATTTG	TGCTTGGCTC	TCTAGCAGCC	TAGCAGAATC	AACAACTCC	AGGTTCAAGT	1140
	AGAGATGCTC	ACAAAATAAA	ATGGAGGAGC	AACCTGAACAC	ACTCAGTGTT	GACCCACACA	1200
	CACACTAATA	AACACAGTGA	CCACACAGAC	ACAGACACAG	GATAACCTAC	CCATGTTGTG	1260
	TATGGACTCA	GCCAGCCGAC	GTTGGAAACT	CAGTTCCTCT	GTTAACCTTT	TTCAACACTG	1320
	GGTCTCCAGC	GATGCTGTGG	GGAACTTACT	TACGGGCAAT	ATTCTGGGCA	TATAGATGAA	1380
30	AGGAAGCAGT	AAAGTTTCCC	TTTCTTGAC	TGAGGTGATG	CGAGAATAGG	GGCCTGAATT	1440
	CCATCTCTAG	GACTTCACATA	AAGTACACCA	GACTGCATCT	GCCAGTAAGC	CTCACCTATG	1500
	CCTCCAAGCC	TGGCTGTGAG	AGAATGTCTC	AAAAACAAG	TAAACAACAC	AAATCAATG	1560
	TCAGATGTGC	ACACATCGAA	TCCAGCATG	TGTACGGCAT	GCTTGCACTC	AGCCTTGTTT	1620
	ACAGAGAGTT	CTAGGCCAAC	CAGCTATACA	CAGTGAGACC	CTGTGGTAGA	CGGCTCTTAA	1680
35	GAACTGACAT	TTGTGACTGA	CAGATGTGCA	CATCTACACC	ATGCACATCA	CAGTTTCCAT	1740
	TTTACAAAAA	GGTTAAACAT	TACTAATTGA	TTAGGGAGTG	GGGCAACCCA	CTGTACATAG	1800
	TGAAGCCGAG	GAAGATGATG	GTTCCAGTCG	GCTAGTTGTG	TGCTTCCACC	ATGTAGGTC	1860
	TAAAAATTGA	ACTCAAGGCA	GTCCTGGCAG	CAAGTGCTTT	ATCCATAGTG	CCATCTTAAT	1920
	GGCCCACTCT	CCTTATAAAT	AAATATTATG	TGTTTCCAA	TTGATGTAAT	TTCTTTAAAA	1980
40	TCAGCTGTGC	TCCTTGGAGT	TTGACTTCAC	TGAAGCCTGT	TACAGGAGTG	CCCTTCTCTC	2040
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	TGGGCTTCCC	TCCTTCATTC	CTCCTGGGCT	CAATGCCAAG	CCGGTTTCCA	TTCTTTTTC	2160
	GTGCACTGCG	AAGAGGCTTT	GGGGAAGCGG	CCTCATCCAT	CATGCAGAGA	GCTCCTCCCC	2220
	CACCTCTACA	GAGAGCCGAC	CAAGCTTGCT	TCCTTGGGCT	TGCTCTGTCC	ACCCTGTGAG	2280
45	GAGGCTGGGA	TGAGGTTGGG	GATGGGGAGG	ATCAGGATCT	AGATGTTTTT	AAGTCTGAGA	2340
	AGCAGGTGAG	CTTGGTCCCT	GAGAATATAT	GAAGGGTCTC	ACTGGGGTTG	AGATATAGAT	2400
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50	GGTAAGTAA	AGCCAGTACT	TGCCCATGGT	CCTGCTGTTA	TAAAGAGGCT	CAGTAGAGCT	2640
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	CTCTGAGTGT	AATATTGGGA	TATTAACAAG	TACTGACCTT	CTGAGGACC	CGGTGGGTAC	2760
	TCAGCTCTTC	TGGCCTGCAA	AATGGGCTTG	GGACAGTTTG	GCCAGGATCA	TCCTCTGGTT	2820
	GGGAGAACCA	CTGTCAAGTG	GGTCTGGAGC	TCTTATTAGT	ACTGGGGTCC	CCATAACGCT	2880
55	CCATGGGCTC	AGCGGGAGGC	TGCACGGGAC	CATATTAGT	CAGGGGGAGC	CAGAGCCCCG	2940
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AGTCAGAGAC	AACCTTGCAGA	AGATGGTTTG	CTCTTTTCAT	CATATGGGCC	CATGGGATTA	13020
AACCTCAAGT	ATCAGTTTIT	GTGCCAACCC	CCTTTACTCC	CCGAGCCTCT	TCTCAACAGC	13080
TCTCTCACTT	ACCTTTTAT	TTAAAAACAA	AACAACACAA	CAAAACACAA	CCAGCCTCTC	13140
CACACAACAA	CGAAAAGATC	TCAATGTAGCC	CCAGGGTGGC	TTTGAACCTC	CCATATAGCT	13200
TAGGATGACT	TTGAATTCCT	AATGTTCTTG	CTCTACCTC	CTAGTTACTA	TGCCGTGCTT	13260
CTTACCATAG	AAATTAAGAA	ATTATCTAAG	GTAAGTGGT	GTTATGTGCT	TATAAGCCAG	13320
GCACCTCAGG	AGAAGCTAAG	GCATGATGAT	TGTGATTTTG	AAGCCAACTC	AGGTTACAGA	13380
GGATCTCATC	AGAAATCTAG	CATTCAATTT	TCAATTTATT	CTTAAATTTT	TTGAGGTTTG	13440
GCTGGAGGGG	TTGGTTAAGA	GCACCTGGTG	GTCTTCCAGA	GGACATGAGT	TTGATTCCTT	13500
GTACCCCAAC	TGGTGGCTCA	CACCACTCTG	TAATTTTAAAT	TCTAGGGATC	TAAAGCCCTC	13560
TTCAAGCCTT	CTCAGGCAGG	TGATATAAGTA	CACAGTCATA	CATGCACAGA	AAACACATAA	13620
ACATAAATAA	AATAAATTAAT	AATTTTGAAA	GTTTTTTTTG	GGTGGAGAGT	ACCTTTAAGT	13680

	AACATTCTAT	GTTATGGAAC	AAGTGCATTC	AATTTTACTA	AGTTTTTAAT	TTTAGCTTTT	13740
	TGTTTGTGTTG	TTTTCTGTGTT	GGAAACAGGT	CTGTGTATC	CCAAGCATCC	TCAAAGTTGT	13800
	TGTGTATGCGA	AGGATGACCT	TGAATTTTTT	TATACTACTG	CCTTCTTGAG	GGCAAGCATT	13860
5	TTAATATAGG	CAAAATAAAC	TTTAAACTTT	GTTTGCTGTG	CAGGTATATA	TGGTGTGCAA	13920
	GTGTATCTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGAGA	GAGAGAGAGA	13980
	GAGAGAGAGA	GAGAGAGAGA	GAGAGAGAGA	GATTAGAGAA	TAACTTGTGG	AAGTTCTCTC	14040
	CTTCTACCTC	TGGGTCCCA	GGGTAAACCT	GGGTATATAAG	GCTTTGCACC	CTTTTCCCA	14100
	CTGAGAACTT	CTTGTCTGGC	TCACTCCCTA	TTTTATTTA	TGGTGGCAG	TACTATTGCT	14160
	TTTGAATCCC	ATCTGAAGCT	TGTTTTGTGT	GTTTGGTTTT	TAAGGCAGTC	TTAACTGTGA	14220
10	CCTAAGCTGG	TTTTAAACTC	ACAGGAATTA	TCCACCTCCA	CCTCCCAAGT	GTTGGGGTTA	14280
	CAGATGTGAG	CCCCAAGCCT	GAGTGTCTCT	GAAAGCTGCT	TTTTTTTATT	TCAAAACCTAT	14340
	CTTTTCTCTG	TGTGTAGGTC	TGATTAGTTG	TGGGGTTAGG	TGGTGTCCAG	ATGATCCATC	14400
	ACTCTCCAGC	TATTATTCTT	AAAATGAAGG	GTCTGGGGGC	TGGGGATTTA	GCTCAGTGGT	14460
	AGAGCGCTTA	CCTAGGAAGC	GCAAGGCCCT	GGGTTTCGGT	CCCAGCTCCG	AAAAAAGAA	14520
15	CCAAAAAATA	AAAAAATGAA	GGGTCTGGTG	GCTGAGGAAA	AAGCTCAGTT	GCAAAAAAAC	14580
	ATGAAAACTT	GATTCAATCT	GTAAGGCCCA	CATAAAGGCC	AGGCATGGCG	GCATGCACCT	14640
	ATAACCCCGA	CACCTGGGAA	ACAGAACAGG	AGAATACCAA	GAACTTCTGT	GTCAGTCAGT	14700
	CTAGTTTAAAT	TGGTGTAGCT	CAAGCTCAGT	GAGACCCGTG	CTCAAAAAAT	AATGGAGATG	14760
	ATCTGTATC	AAGACCTGGC	CTCCATACAT	ATATGCACAC	ATGTTACTCC	CTCACATGAA	14820
20	ACATATTTAT	AAACAAACAT	ATGCACACAC	TTGTGCATAC	ATGAACAGAT	ATCTATATTG	14880
	GCATACACAT	TAAAAACACAT	ACACACATAT	ATATATACAA	AAGTGTGTAC	AAACATAGGC	14940
	ATAGTATACA	ACCATGCATA	AATGCACAGT	CACACATATG	AATGCATTCA	TATTCACACA	15000
	TGGACACATC	AACACATATA	TATATGCTAT	ATCTTATATT	ACACTCCATT	ACTATCCCCC	15060
25	AGTCCAGGTT	TCAAATATTT	ACAAACAGAA	AAGCGGGCTA	CTACCTGTAC	TCTTTCCCAA	15120
	TTCGCTTTGA	ACAGCGATCT	CTCGACACCT	GATCCCCGCA	GTGCTCCCTG	CGGCAGAGCT	15180
	TCATCCGGAA	ACAAACCCCA	TGCACCTCTAT	TGATTTTAAAT	ACTGGGGATT	ACCTGGGAGC	15240
	TGTAAAGCT	AAACACATTG	TCTACTGCTA	AATACTTTCAT	TCTTTGCCCC	TTTCCCATGG	15300
	GGCGTTTTC	ATCCAGTTAT	TTTGTAGTGT	TTCTTAGATT	TAAGCATCCA	CTAGTACAGA	15360
	TTCAAGGATA	TTTTTATTAT	CCCCCAAATA	ACAGTATTGT	TTAGGTGTAA	CCTGTGTAGT	15420
30	TTTCCCCAGC	GGCTAATTTA	AATTGCTTTC	ATGAATAGCC	TATTCTGAA	AAGTAATTTT	15480
	TTTTTTTTTT	TTTTTTTTTG	GGTCTTTTTT	TTGCGAGCTG	GGGACCGAAC	CCAGGGCCTT	15540
	GCCTCTCCTA	GGTAAGCGCT	CTACCACTGA	GCTAAATCCC	CAGCCCCAAT	CTTGGACATT	15600
	TCTTATAAAT	GTCACATATC	TGTATGTGTT	CTTTCAGCAT	TGCAACACTT	TGGTTCCTTT	15660
	TTATGGCTCA	ATACTGGTCT	ACTTATGGAT	CTACCACACT	ATCTATCCAT	TCATCTCAAC	15720
35	ATAGTCATGG	GTGGTATTTT	TACTTTGGGG	CTATTATAAG	CTTGCTAGGA	GTATTTATGA	15780
	CCACATCTTT	AGATGCACCTG	ATGCATTCAT	TTATCCTAAG	AACAGATCCG	GGATCATATG	15840
	GTGGTCTCTG	GTTCAAAACAT	CAGAGGCCAC	ACCATTATT	TTATAATAGG	CAITTTAAGAT	15900
	TGCGGTATCT	TCTAACTGGG	TGGTGGTGGT	ACATGCCTGT	AGTCCCAGCT	CCTGGGAGGC	15960
40	AGAGGCAAGT	AGATCCGAAT	TCTCGCCCTA	TAGTGAGTCG	TATTAGTCGA	C	16011

+11,795 (1st intron)

# SEQ ID NO:17

## The 5' (-5086) and 3' limits of the Human SM-MHC Promoter-Enhancer LacZ Transgene Tested in Transgenic Mice

5 The number in the left margin refers to the position within an undefined BAC sequence contained in the public database (Accession # U91323 in GenBank). The start site (i.e. +1 position) of the SM-MHC gene corresponds to the BAC position 143,590.

-5086 TTTAAA ATTATTAAAT CTTCTTTTTT TTTTTTTTGA

10	138541	GATGGAGCCT	CTCTCTCTAG	CCTAGGCTAG	AGTGCATAGG	TGTGATCTTG	GCTCACTGCA
	138601	ACCTCCACCT	CCCAGGTCTA	AGGAGTCTCT	CTGTCTCAGC	CTCCCAAGTA	GCTGGGACTA
	138661	CAGGCGTGCA	CAACCACACC	CGACTAGTTT	TTGTATTTTT	AGTAGTGATA	GGGTTTTACC
	138721	ATGTTGGCCA	GGCTGGTCTC	GAACTCCTGA	CCTCAAGTGT	TCCTCCACC	TTGGCCTCCC
	138781	AAAGTGCTGG	GATTACAGGT	GTGAGCCACT	GTGCGCGGCC	AAAAAATATT	AAATCTTGAG
15	138841	GCACATGCAG	GAGTAAGCCA	TGCTCAGACC	CAATCTTCGA	TGTTACTAAA	AATTGGAGGG
	138901	GATCACACTT	CATGGTTTTG	TTTTGTTTTG	TTTTTTTGAG	ACAGGGTCTT	GCTCTGTTGC
	138961	CCAGGCTGGA	GTGCACATGT	ACGATCAGAG	TTCACTGCGA	CCTCAAACTC	TGGGGCTCAA
	139021	ACAATCCCTC	TACTTCACTC	TCTAGTTGGG	ACTACAGGCA	CACACTGCTG	GTCTCGACTA
	139081	ATTATTATTA	TTATTATTAT	TATTATTATT	ATTATTATTA	TTATTATTAT	GTAGAGACAG
20	139141	GGATCTTGCT	ATGTTACCTA	GGCTGTTCTT	GAACTCCTGG	GCTCAAGCGA	TCCTTCGCGT
	139201	GCAGCCTCTC	AAAGTGTCTAG	GATTACAGGC	AGCTTCGGGC	ACCTTCGGGC	TTTTTTAAGC
	139261	CAACAGCAAA	AAAAGACTAT	AAGAGAGAAA	TTTCCCTTGG	GCTGTCTTGT	TTCACTGGAT
	139321	CGTGGAAACT	CCCATTAAAC	AGCCGCTCAC	AGAAAAGAT	ATGCCAAGGA	AAATTTACTT
	139381	ACAGCATCTA	GTCAAAAGTA	CATTTTAAAA	AGAGACTATT	GCCTCCTCCA	TCTTAAAAAG
25	139441	ACTGACCTTT	TGAGCCATGA	GAAATGAAAC	AGAGGCATCT	GATCGAATGA	TAACAATGCA
	139501	CTTCTGAAGA	TCTAAACATC	GGAATTCAT	GCATTGGACA	CATATCTATT	GAATGACTCT
	139561	TAAGTGAACA	TACTGTCCCT	GCCTGTCTCC	GAGGTGTAAT	GAGATGGTCC	GAGATGGTCC
	139621	ATAAGGCGCT	TCACATGTGC	TGTCATATTT	AACAATCAGA	AAGGTACTGT	AGGCAATGCA
	139681	TCTGATCACT	TTTGTTTTTT	CTTGAGAAAA	TGCGCTCAGA	GAGGTTTACT	CAACAACCCA
30	139741	AAGGTGCTGT	TGTGGTGCTT	AAGAGATCTG	GGTTTAAAA	CTCAGACTGC	TGCTACTACT
	139801	GGCCTGTGTC	AGAAAGACTG	GGGTGTGAAT	TCCTGTCCCA	CCACTGTCTG	GTATTTTAA
	139861	CCCTCCAAAC	CTAGATTCTC	AACAATAAAA	TGGGGGTAGG	GAGGGAATTA	AAGTATGTAC
	139921	CTTATTTTTT	AGAGACAACA	TCTTGCTCTG	TCGCCCAAGC	TAGAGTGCAG	TGGTGCAATC
	139981	ATAGTTCACT	TAGTCTCAA	CCTTCCAAGC	TCAAGAGATC	CTCCTACCTC	AGCCTCCCTA
35	140041	GTAGCTGGAA	CTTCAGGCTA	CACCTACGCC	AGCTGCTATT	TATTATTTAT	TTATTTATTG
	140101	AGATTGCATC	TCACCATGTT	GCCCAGGCTG	GCTACTTAAA	AAAAATTTTT	TTTTTCAAGA
	140161	CAGGCTCTCA	CTCTGCCACC	CAGGCTGGAG	TACAGTGACA	GAGTCTCAGC	TGCTGCAAC
	140221	CTCTGCCTCC	CAGGCTCAAG	TGATCTTCCC	ACCTCAGCCT	CCCAAGGAGC	TGGGATATCA
40	140281	GGTACCACC	ACCACACATG	GCTAACTTTT	TATTTTGTGT	AGAGACAGGG	TCCTGCTATG
	140341	TTGCCCAAGC	TGGTCTCAAA	CTCTCGAGCT	CAAGCAATCC	TCTGCTTTTG	GCCTCCCAA
	140401	GTGCTAGGAT	TACAGTTGTG	AGCCACCATG	CTGGGCGTTG	GCCACTTTAG	TTTTGCTTTT
	140461	TTTTTTTTTT	TTTGAGTTGG	AGTCTTGCTC	TGTCATCCAG	GCTCCCAAGC	TGGAGTCGAG
	140521	TGACACATCT	TCACCTCACT	GCAACCTCTG	CTCTCTGGGT	TCAAGCAATT	ATCTCTGTAC
45	140581	AGCCTCCCAA	GTAGCTGGGA	CCACAGGTGT	GCACACCAT	GCCCAAGCTA	TTTTATATTT
	140641	TTTAGTAGAA	ATGGGGGTTT	CACCATGTTG	CTTAGGCTGG	TCTTGAACCT	CTGACTTCAA
	140701	GTGATCGCGC	TACTTTGGCC	TCCCAAAGTG	CTGGGATTAC	AGGCAAGAGC	CACGCTGCC
	140761	GGCTGCCTAC	TTTAAATTTT	AATAAAGGGT	TGTTATATAA	GGGCTAGGTG	AGAGAATGAA
	140821	GTAAAAATTGA	GTGTTACAGT	CTCCAGTTGT	TAACTACATT	ATAAATATT	TCCTTTAAAA
	140881	GTAAACCAACA	AGTTATTAAA	AGAATCGAAT	GGAACCCCTT	GGAATACAG	GTGTCATGCC
50	140941	TCTAGTATTA	ATGCCAGTTT	TTACTTCGAG	GCCAGCAAGC	TAGATTCCGA	TGGCCTTCCC
	141001	TTTCCAGGAT	GGGAAGCGGA	TGATTGACTT	CAATTTTCCC	CCTTCCGTTA	CTTCTCTGCT
	141061	CCACATCATT	TCTGTGCTGA	TGCAGGGAGC	ATTTCACCTC	CTTTTACAGC	GATGATGTTA
	141121	AAAGCCTGTG	CGGAGCAGCT	CATTTCATCT	TTTCCGAGAG	GCTTTTACCC	CTACTTCCCC
	141181	AGCCAGCTAA	ATGAGGCGTG	TTCTTGACTC	TCTTGATCTAG	GCCCATTTGCA	GGGTGAGGCG
55	141241	CAGGCTCAGG	AGTTTCCAGG	GTGAAAACCA	CCTAAGCTTG	ATGTTGGAAG	GATGAAGGAG
	141301	GACCCAAAAG	GGTCTGAGAT	GCAGAGCTCT	CTGGAGGCGC	CTGGGAGGAG	CAGGCGGAAG
	141361	AGGCTCTCT	TTATATCCCG	GAGGCTCTGT	GCAACTCTAG	TGTGTTTCAT	GTGTTGTTGC
	141421	AGTAACAGCA	GCTCACATGA	AGCGGTGCAC	CATGTTTCATT	TTACATGGAT	TCATCTCAAG

141481 GACTGCTTAC AAAAAGGCCA GGAAGTAGCT GATGTTCTTC CCACTTTACA GGTAGGGAAA  
141541 TTGAGGCATG GAGAGGCAAA GTTACTTGCC CATGGTCATA TAGGTAGAAA GCAGCACTGG  
141601 CAGATTCAAA CCCAGACATC TACTCTCAGA TACACGCCCT GGGCTCTCAAG GCCACTTTGC  
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141721 AGTGCCACGA CCAATCAATG ACTGTCCGAG TGAGAGAGTT GTCAAAATCCC TTTACCCCTG  
141781 CAGGAGCTCA ATTTTCTCAC CTGCAAAATG GGGGTATTAA TAAAGGCCACC CCCGCCACCC  
141841 CGCGCCCCCA GCCCTCCAC CTGGTTGCAA GAGGAGTGGT TGATAGACTAA GGGCTGTGGT  
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141961 TGAAGACAGA GAAACCCAGG TGGGACTGGG GGCCTGCCCC TTCCCGGCCCT TCCCAACAGA  
142021 GAGGGGTCC CATCTAGCCC CGCGGGGCAA CGCGGGCGG GGTGTGGCTG AAGGGCCCCC  
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142141 CAGCCAGAG CTGGTATGG CGCCTGGGAA AGCCCTGCGG TTCTGTGAGG AAGGAGTCCG GCCTGTCCCT  
142201 TTTTGGGTTG TCTCCGCCCC GCGCTTCCCG CCGCTCCCGG GAGAGGGGAC CGCCCGGGCT  
142261 CGCGCCGGCC CGGGAACCTC GGAGGAGCTG GTGCGCGCGG GGGAGCGGAG CTGCAGCTTC  
142321 GCGCGCGGTT CCCCGCCTG CGCGCGGGCC AGCCCAACGC CTCGACTTCC TTTTATGGCC  
142381 TGTGTGTGCG TGCGTGGACA GGAGCGGGGA GGGAGGGAGC GGGAGAAAGC GGAGAGCGCT  
142441 GGGAGAGAGC AGAGAGAAAG CGCAGAGATA GGAGTGAGAG ACGCGGGAGA GATGGAGAGC  
142501 AAGAGACAGA GAGACCAGAG ACAAGTGAAG ACAGAGGGGA GAGACAGATA CATCGACAGA  
142561 TCTAGAGAGA GAGAGGGGAC AGAGACAAAA GATTAGAGCA GAGACAGCAA TGATCAGAGT  
142621 GACAGACATG CAGAGACAGT GGCAGAGACA GAGCAGAGAG GCGCTGTGAT GAGAGAGACA  
142681 GGGAAATGCA TTTTAGCGCA GGAATCCTTG GGAAGGGAAA GTTGTTTAAG GGAATCGCA  
142741 GACTCTGGGG GTACAGCCCA TTTCTCCTTG GATCTTGACA CTTCGATCTT GTAATAACG  
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142981 GGTGGAGGTG GAGATGGCAA GTTGGGAAAA GTTAAACACT CCCCTTCTCG CACGTTTCCC  
143041 AGCAAGGTGG GGGGCTTCTT GTCTTGCACT TTGCAAAAGT CAGAAGAAATC CCTTTCCCTA  
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143161 TGGGGTGGGA GATGTCAAGT CAGATCCACC ACAGCCCGGA CACGGGGAGG AAGAGGTTAA  
143221 AGCCTTTTGG CGCCTGAACC ACTCAGGAA GAGCTTCTCA AGCATCCCGC ACAGACATG  
143281 CTGCTCTGAC CCCCTTTCTC TAGGGATCCG GAGCGTCTGC GACCCTCTGG GCGCCGGGCT  
143341 GAGACTCCCG TCCCTGTGCG CACCTGTTCG GTGCGCTCCC GTGCGGTGCG CACCTGTTCG  
143401 GTGACCCCTT TTCCCGAGCG CCCAGCTCC TTGCGCTCCC GCGCGGGGCT GCGCCTGCGC  
143461 GGGGCGCGCG GAGGGGGCG CGAGGGACCC TCCCAACCT CACCCCTTCG CCGCTCTCCC  
143521 CTTTCCGAGC CGCGGGCAGC TCCGGTCTTA TAAAGAGAGG CGTCTCGAGA GCGCTCGGGA

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143581 GATTTGGAGC CTCCGCGCTG GAGGTTGCGT CAGATCCGAG CTCGCCATCC AGTTTCTCTT  
143641 CCACTAGTGG CCCCACTTGG AGATCTGTAA GTAGTAGTTG TCATCTTGGG GGCAGATTGC  
143701 AGGGCAGGGG GGTGTTAAAA GTCTATAGG GTATCTTATG GGGGCTGGG TGCCTTAGG  
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143821 CTCTGCCCTA TCGTCTTAGA TTATCTTAGA CTITCCCAA ACAGCACTTC TTAAGATTGC  
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144061 TGCAAGCAAT CAAAGCATCT CACTTTTAT TTAGGCACCA AAAAATTTAC AGCTGAACCT  
144121 CACTGAAAAA GAGTGTGCTA TCACACAGAA GGCACAAAGT AGGCTCCTTG TGTATTGAGC  
144181 CGTATTGACG AGTGTGTTG ATAATGCATT AAATCAGTTA AAACACATG TACGATAGCT  
144241 TGAAGAAGAG GAGTGTGTT GTTTTTTTT TTTAATCAGT TTAGGGGAGG TTCTTCTATG  
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144481 AGATTACACT AGAATTTCCC CGACAGCCAC CTGTGTCAAT GCGACTCTCG TCCCAACCA  
144541 AATGGGTAAA AGCAGAGAAA GTGTGGCTAC TGCCTGTTGT AAGTTTCTCT CCAGCACAGG  
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145141 AAGTTTCATC CCTTGCACCC ACTATCTTTT TTCTTTTACCA TGGACACAAA CTTTGTTGGGG  
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145321 TTGAGGGGGT GACCTAGCTG AAACCAAGTGA CCTAGGTGG GCTGGCATGG CGAGAGTCCA  
145381 GAACGTGAAC TAGCTGGGCT TTTTCCGAGA AGCCGCGCAG CTGTGCTTGT AAACACCAATG  
145441 TTTTTTTTAT ATCATGTCCG AAATAGATGT GTTATTCOGT ACAGAGTATC TGTATTGATG  
145501 TTGTATATAT TACTTTTCCG TGGGAGGGCA GAGATTGAGG CAACATGTGC CATTATTGGA  
145561 AGCGTTTTC ATGAGGCCAT CCCCAGCCCC CTCGTCAAGT ACCCAGCCTT GCACCGCAGC  
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145741 CTTATTTCAGA GGTTTGATTT TTTTGGGTGG GGGGTGGGAG GGAATTGTCT CTTTCCACA  
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147121 CAACCTTCATC AAGTGTGCTA GGAAGAGGCC ATAGAGGCCA GGTATGCGAG GTCATACCTG  
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147481 GGCTGAAAAA TACTGAGCCC AGAGAGGGCA AGTAGCTTGC CTAGCATCAC CCAGCAGATT  
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